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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 s
                                                                                                                                            Minimum DB
Maximum DB
                                                         Database
                                                                                                                                                                                   Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                          Scoring table:
                                                                                                                                                                                                                                                                                                  Title:
Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                  OM protein - protein search, using sw model
                                                                                                                                           seq
                                                                                                                                         length: 0
length: 2000000000
  2:
                                                                                                                                                                                                                                                                                                     US-09-331-631A-24_COPY_29_94
382
                                                         PIR_66:*
                                                                                                                                                                                                                 195891 seqs, 67900655 residues
                                                                                                                                                                                                                                           Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                         March
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pir1:*
pir2:*
pir3:*
pir4:*
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                                                                                                                                                                                                                                                                                                                                                                      2001, 16:10:43; Search time 32.86 Seconds
                                                                                    summaries
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Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                          (without alignments)
136.380 Million cell updates/sec
                                                                                                                                                                                    195891
                                                                                                                                                                                                                                                                                     66
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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29	28	27	26	25	24	2 3	22	21	20	19	18	17	16	15	14	13	12	11	10	9	00	7	6	ر ت	4	ω	2	L	No.	Result	
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T30251	A25018	B26427	S52943	S52941	T06459	S71512	S37241	A34373	S22477	S27770	S20007	FWSYBA	T44430	T13998	T06453	S04321	S06398	B24810	FWCNAB	61	S08059	9	23	23	82	T02258	B53234	S35221	ID		
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ALIGNMENTS

globulin Beg1 precursor - barley
C:Species: Hordeum vulgare (barley)
C:Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 21-Jul-2000

R; Heck, G.R.; Chamberlain, A.K.; Ho, T.H.D. Mol. Gen. Genet. 239, 209-218, 1993

C; Accession: S35221

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vicilin-like storage protein Glb1-L, embryo - maize N;Alternate names: globulin-LL C:Species: Zea mays (maize) C:Date: 02-May-1994 #sequence_revision 18-Nov-1994 #text_change 24-Nov-1999 C:Accession: B53334; S21824 R;Belanger, F.C.; Kriz, A.L. Genetics 129, 863-872, 1991 A;Title: Molecular basis for allelic polymorphism of the maize Globulin-1 gene. A;Reference number: A53234; MUID:92090707
A;Molecule type: DNA
A;Residues: 1-582 <BEL>
A;Cross-references: EMBL:X59083; NID:g22283; PIDN:CAA41809.1; PID:g22284
A;Experimental source: inbred line W64A6
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C;Keywords: glycoprotein
F;174-190/Product: globulin Beg1 #status predicted <MAT>
                                                                                     A; Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Map position:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Molecule type: mRNA
A; Residues: 1-637 <HEC>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mol. Gen. Genet. 239, 209-218, 1993
A;Title: Barley embryo globulin 1 gene, Begl: characterization
A;Reference number: S35221; MUID:93287988
A;Accession: S35221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Gene: Beg1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Cross-references: EMBL:M64372; NID:g167003; PIDN:AAA32936.1; PID:g167004
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Best Local S
Matches 66
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66; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100.0%; llarity 100.0%; Conservative 0
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Pred. No. 1.8e-32;
; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 637;
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vicilin-like storage protein Glb1-S, embryo - maize
C:Species: Zea mays (maize)
C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 11-Jan-2000
C;Accession: S21825
R;Kriz, A.L.
submitted to the EMBL Data Library, April 1991
A;Reference number: S21823
A;Accession: S21825
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-540 <KRI>
A;Cross-references: EMBL:X59084; NID:g22285; PIDN:CAA41810.1; PID:g22287
C;Genetics:
A;Genetics:
A;G
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C:Species: Zea mays (maize)
C:Date: 05-Mar-1999 #sequence_revision 05-Mar-1999 #text_change 29-Oct-1999
C:Accession: T02258
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A;Introns: 167/1; 225/3;
C;Superfamily: glycinin
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C; Genetics:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Experimental source: strain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Cross-references: EMBL:U28017; NID:g927238; PIDN:AAB60295.1; PID:g927239
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Reference number:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Description: Nucleotide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         submitted to the EMBL Data Library, May 1995
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Best Local S
Matches 25
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   58 WHGEGEREE 66
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DDEDDRRGGHSLQQCVQRCRQERPRYSHARCVQECRDDQ----QOHGRHBQEEEQGRGRG 57
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l Similarity 36.2%;
25; Conservative 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                92
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Pred. No. 4.3e-07;
_4; Mismatches 21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 135; DB 2;
Pred. No. 6.3e-07;
6; Mismatches 22;
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globulin-10 - maize
C:Species: Zea mays (maize)
C:Date: 02-May-1994 #sequence_revision 18-Nov-1994
C:Accession: C53234; S21823
R:Belanger, F.C.; Kriz, A.L.
Genetics 129, 863-872, 1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C;Species: Zea mays (maize)
C;Date: (02-May-1994 #sequence_revision 18-Nov-1994 #text_change 11-Jan-2000
C;Accession: A53234; A43642
R;Belanger, F.C.; Kriz, A.L.
Genetics 129, 863-872, 1991
A;Title: Molecular basis for allelic polymorphism of the maize Globulin-1 gc
A;Reference number: A53234; MUID:92090707
A;Residues: 1-122 <BEL>
A;Cross-references: EMBL:X59085; NID:g22281; PIDN:CAA41811.1;
A;Note: sequence extracted from NCBI backbone (NCBIN:71282, NC
                                                                                                                   A; Title: Molecular basis for allelic polymorphism of A; Reference number: A53234; MUID:92090707 A; Contents: Black Beauty popcorn
                                                                              A; Accession: C53234
A; Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A:Status: preliminary
A:Molecule type: protein
A:Residues: 87-100 <KRI>
C:Superfamily: glycinin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Molecule type: DNA
A; Residues: 1-573 <BEL>
                                                           A; Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Reference number: A; Accession: A43642
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Note: sequence extracted from NCBI backbone (NCBIN:71280, NCBIP:71284) R;\mbox{Kriz},\mbox{ A.L.}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Title: Characterization of
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Experimental source: inbred line Va
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 36.2
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Best Local Similarity
---hes 25; Conservative
                                                                                                                                                                                                                                                                                                                                                                                        85
                                                                                                                                                                                                                                                                                                                                                                                                                             58 WHGEGEREE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                26 DDNHHHHGGHKSGRCVRRC-EDRPWHQRPRCLEQCREEEREKRQERSRHEADDRSGEGSS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 58 WHCEGEREE 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2 DDEDDRRGGHSLQQCVQRCRQERPRYSHARCVQECRDDQ----QQHGRHEQEEEQGRGRG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2 DDEDDRRGGHSLQQCVQRCRQERPRYSHARCVQECRDDQ----QHGRHEQEEEQGRGRG 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Genet. 27, 239-251,
                                                                                                                                                                                                                                                                                                                                                                                        -EDEREREQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 zation of embryo globulins encoded A43642; MUID:89374022
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Pred. No. 1.4e-06;
"'~matches 23;
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Pred. No. 1.3e-06;
5; Mismatches 23;
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                                                                                                                                                               maize
  l; PID:g22282
NCBIP:71286)
                                                                                                                                                             Globulin-1 gene
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A; Residues: 1-509 <CHL>
C; Superfamily: glycinin
                                                                                                                                                                                                                                                                                        A; Reference number: S06398
A; Accession: S08059
                                                                                                                                                                                                                                                                                                                       R;Chlan, C.A.; Borroto, K.; Kamalay, J.A.; Dure III, L. Plant Mol. Biol. 9, 533-546, 1987
A;Title: Developmental biochemistry of cottonseed embryogenesis
                                                                                                                                                                                                                                                                                                                                                                                           alpha-globulin type B precursor (tandem 1) - upland cotton (fragment) N;Alternate names: seed storage protein C;Species: Gossypium hirsutum (upland cotton) C;Date: 31-Mar-1990 #sequence_revision 31-Mar-1990 #text_change 30-Se
 Вb
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                                                                                                                                                                                                                                                                          A; Status: not compared with conceptual translation
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Introns: 166/1; 224/3 C; Superfamily: glycinin
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Cross-references: EMBL:AF064222; NID:g3414836; PIDN:AAC31465.1; A;Experimental source: subspecies parviglumis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Molecule type: DNA
A; Residues: 1-236 <HIL>
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Genetics 150, 863-872, 1998
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C;Species: Zea mays (maize)
C;Date: 19-Feb-1999 #sequence_revision 19-Feb-1999 #text_change 11-Jan-2000
C;Accession: T01662
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Best Local
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Best Local :
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                                 HGEGEREE 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DDNHHHHGGHKSGRCVRRC-EDRPWHQRPRCLEQCREEER--SRHEADDRSGEG---SSE 79
                                                                  EQEQQQSQRQFQECQQHCHQQEQRPEKKQQCVRECREKYQENPWRGEREEEAEEEETE--
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-EGEQEQ
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22; Conserv
                                                                                                                                                    Similarity
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                                                                                                                                      Conservative
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96
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37.5%;
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37.9%;
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Pred. No. 2.6e-06;
                                                                                                                                                    Score 93; DB 2; Pred. No. 0.018;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 129.5; DB 2;
Pred. No. 7.8e-07;
3; Mismatches 18;
                                                                                                                                    Mismatches
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                                                                                                                                Gaps
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A;Molecule type: mRNA
A;Residues: 1-588 <CHLD
A;Cross-references: GB:M16891; NID:g167374; PIDN:AAA33071.1;
A;Cross-references: GB:M16891; NID:g167374; PIDN:AAA33071.1;
A;Chlan, C.A.; Borroto, K.; Kamalay, J.A.; Dure III, L.
Plant Mol. Biol. 9, 533-546, 1987
A;Title: Developmental biochemistry of cottonseed embryogenes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Cross-references: GB:M21759; NID:g204143; PIDN:AAA41161.1; PID:g204144 A;Note: the authors translated the codon GAA for residue 568 as Gln C;Superfamily: unassigned calmodulin-related proteins; calmodulin repeat homology C;Keywords: EF hand; epidermis
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                                                                                                                                                                                                                 F;1-25/Domain: signal sequence *status predicted <SIG> F;26-588/Product: alpha-globulin storage proprotein *status predicted F;417/Binding site: carbohydrate (Asn) (covalent) *status predicted
                                                                                                                                                                                                                                                                                            A;Residues: 1-81 <CH2>
C;Comment: This is a seed storage protein.
C;Superfamily: glycinin
C;Keywords: glycoprotein; seed; storage protein
                                                                                                                                                                                                                                                                                                                                                                                              A; Molecule type:
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A; Accession: A30838
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R;Chlan, C.A.; Pyle, J.B.; Legocki, A.B.; Dure III, L.
Plant Mol. Biol. 7, 475-489, 1986
A;Title: Developmental biochemistry of cottonseed embryogenesis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      alpha-globulin B precursor (clone C72) - upland cotton N;Alternate names: seed storage protein; vicilin precursor C;Species: Gossypium hirsutum (upland cotton) C;Date: 30-Sep-1991 #text_change 16-Jul-1999 C;Date: 30-Sep-1991 #text_change 16-Jul-1999
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DNA Cell Biol. 9, 251-261, 1990
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C;Species: Rattus norvegicus (Norway rat)
C;Date: 29-Jun-1990 #sequence_revision 09-Oct-1992 #text_change 04-Feb-2000
C;Accession: A34615
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A34615
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Reference number: S06398
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A; Residues: 1-625 <HAY>
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                                                                                                    Matches
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Best Local :
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Best Local
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                                              3 DEDDRRGGHSLQQCVQRCRQERPRYSH-ARCVQECRDDQQQH-GRHEQEEEQGRGRGWHG
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EQEQQQSQRQFQECQQHCHQQEQRPERKQQCVRECRERYQENPWRREREEEAEEEETEEG 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EDESDAQQGHQQQQQQR-QQQRQRQQHE----QEREHEQQQPESSQRQQGSSGRTQRAAR 374
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                                                                                                                      23.6%;
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35.1%;
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                                                                                                                      Score 90; DB 1;
Pred. No. 0.043;
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                                                                                                  Mismatches
                                                                                                  28;
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                                                                                                                                              Length 588
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A:Status: not compared with conceptual translation
A:Molecule type: DNA
A:Molecule type: DNA
A:Residues: 1-605 <CHL>
C:Superfamily: glycinin
F:1-24/Domain: signal sequence #status predicted <SIG>
F:25-605/Product: alpha-globulin type A #status predicted <MAT>
                                                                                                                                                                                                                                                                                                                                                          alpha-globulin type A precursor - upland cotton
Alpha-globulin type A precursor - upland cotton
N.Alternate names: seed storage protein
C.Species: Gossypium hirsutum (upland cotton)
C.Date: 31-Mar-1990 #sequence_revision 31-Mar-1990 #text_change 30-Sep-1993
C.Accession: S06398
R.Chlan, C.A.; Borroto, K.; Kamalay, J.A.; Dure III, L.
Plant Mol. Biol. 9, 533-546, 1987
                                                                                                                                                                                                                                                                                                 A;Title: Developmental biochemistry of cottonseed A;Reference number: S06398 A;Accession: S06398
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Title: Closely related families of genes code A;Reference number: $16337; MUID:83143288
A;Recession: $16337
A;Molecule type: DNA
A;Residues: 361-639 <SCH>
C;Genetics:
C;Genetics: 278/1; 355/3; 382/3; 481/3; 575/1
C;Superfamily: glycinin
C;Keywords: seed; storage protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 beta-conglycinin alpha chain precursor - soybean c;Speciles: Glycine max (soybean) C;Speciles: Glycine max (soybean) C;Date: 07-Mar-1988 #sequence_revision 30-Jun-1991 #text_change 20-Aug-1999 C;Accession: B24810; S16337 R;Doyle, J.J.; Schuler, M.A.; Godette, W.D.; Zenger, V.; Beachy, R.N.; Slig
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A:Cross-references: GB:M13759; NID:g169928; PIDN:AAB01374.1; PID:g169929 A;Note: the authors translated the codon GGT for residue 352 as Glu R:Schuler, M.A.; Schmitt, E.S.; Beachy, R.N. Nucleic Acids Res. 10, 8225-8244, 1982
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A; Residues: 1-639 < DOY>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  J. Biol. Chem. 261, 9228-9238, 1986
A;Tittle: The glycosylated seed storage proteins of Glycine max and Phaseolus vulgaris.
A;Reference number: A24810; MUID:86250867
A;Accession: B24810
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Best Local S
Matches 26
                                                                                  Ouery Match
Best Local Similarity
                                                                   Matches
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| | :
174 EQEQ 177
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SHNKCLRSCNSEKDSYRNQACHARCNLLKVEEEEECEEGQIPRPRPQHPERERQQHGEKE 93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
26; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Schuler, M.A.; Godette, W.D.; Zenger, V.; Beachy, R.N.; Slightom, J.L.
                                                                 Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 22.3%;
                                                                                  21.9%; Score 83.5; DB 26.0%; Pred. No. 0.21;
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Pred. No.
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                                                                                                      Length 605;
                                                               Indels
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                   ----HGRHEQE 49
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                                                               19;
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                                                               Gaps
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probable legumin B - garden pea
C;Species: Pisum sativum (garden pea)
C;Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 20-Jun-2000
C;Accession: T06453
R;Bown, D.P.
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C; Accession: SU4321
R; Domoney, C.; Barker, D.; Casey,
R; Domoney, C.; Barker, D.; Barker, D.;
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S04321
legumin
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C;Superfamily: glycinin
C;Keywords: seed; storage protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Molecule type: mRNA
A;Residues: 1-566 <BOW>
A;Cross-references: EMBL:X67424; PIDN:CAA47809.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Reference number: Z15688
A;Accession: T06453
A;Status: preliminary; translated
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C;Superfamily: glycinin
F;1-61/Product: legumin B alpha chain (fragment) #status
F;162-338/Product: legumin B beta chain #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 submitted to the EMBL Data Library, June 1992 A; Reference number: Z15688
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A; Residues: 1-338 < DOM>
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C;Species: Pisum sativum (garden pea)
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Best Local S
Matches 20
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Best Local Similarity 22.7
Matches 20; Conservative
   340
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RSYETRRKWKKHTAEKERESHGQGEEEE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL: M16890; NID: g169120;
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22.7%; Pred. No. 1.1;
cive 17; Mismatches
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Pred. No. 0.66
17; Mismatches
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   367
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1.1;
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RESULT 15
13398 gene mastermind protein - fruit fly (Drosophila virilis)
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